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Payne, Jewel
Narva, Kenneth
Foncerrada, Luis

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<151> 1998-05-12

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<151> 1990-08-10

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Thr Met Asp Asp Ile Gln Ser His Gly Gly Phe Asn Lys Val Asp Ser
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Gly Leu Ile Lys Lys Phe Thr Asp Glu Val Leu Ser Leu Asn Ser Phe
 180 185 190

Tyr Thr Asp Arg Leu Pro Val Phe Ile Thr Asp Asn Thr Ala Asp Arg
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Thr Leu Leu Gly Leu Pro Tyr Tyr Ala Ile Leu Ala Ser Met His Leu
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Met Leu Leu Arg Asp Ile Ile Thr Lys Gly Pro Thr Trp Asp Ser Lys
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Pro Ala Asp Leu Thr Ala Tyr Glu Gln Leu Leu Lys Asn Leu Glu Lys
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Pro Pro Pro Asn Ala Lys Asp Ile Phe Glu Ala Met Lys Pro Ala Ile
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Gly Leu Ile Lys Lys Phe Thr Asp Glu Val Leu Ser Leu Asn Ser Phe
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Tyr Thr Asp Arg Leu Pro Val Phe Ile Thr Asp Asn Thr Ala Asp Arg
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Thr Leu Leu Gly Leu Pro Tyr Tyr Ala Ile Leu Ala Ser Met His Leu
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Met Leu Leu Arg Asp Ile Ile Thr Lys Gly Pro Thr Trp Asp Ser Lys
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Ile Asn Phe Thr Pro Asp Ala Ile Asp Ser Phe Lys Thr Asp Ile Lys
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Asn Asn Ile Lys Leu Tyr Ser Lys Thr Ile Tyr Asp Val Phe Gln Lys
 260 265 270

Gly Leu Ala Ser Tyr Gly Thr Pro Ser Asp Leu Glu Ser Phe Ala Lys
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Lys Gln Lys Tyr Ile Glu Ile Met Thr Thr His Cys Leu Asp Phe Ala
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Arg Leu Phe Pro Thr Phe Asp Pro Asp Leu Tyr Pro Thr Gly Ser Gly
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Asp Ile Ser Leu Gln Lys Thr Arg Arg Ile Leu Ser Pro Phe Ile Pro
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Ile Arg Thr Ala Asp Gly Leu Thr Leu Asn Asn Thr Ser Ile Asp Thr
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Ser Asn Trp Pro Asn Tyr Glu Asn Gly Asn Gly Ala Phe Pro Asn Pro
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Ala Gln Tyr Gly Gly Leu Leu Gln Pro Tyr Leu Trp Ala Ile Glu Val
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Gln Asp Ser Val Glu Thr Arg Leu Tyr Gly Gln Leu Pro Ala Val Asp
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Pro Gln Ala Gly Pro Asn Tyr Val Ser Ile Asp Ser Ser Asn Pro Ile
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Ile Gln Ile Asn Met Asp Thr Trp Lys Thr Pro Pro Gln Gly Ala Ser
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Gly Trp Asn Thr Asn Leu Met Arg Gly Ser Val Ser Gly Leu Ser Phe
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Ala Asp Thr Ile Tyr Ser Leu Pro Ala Thr His Tyr Leu Ser Tyr Leu
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Tyr Gly Thr Pro Tyr Gln Thr Ser Asp Asn Tyr Ser Gly His Val Gly
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Ala Leu Val Gly Val Ser Thr Pro Gln Glu Ala Thr Leu Pro Asn Ile
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Ile Gly Gln Pro Asp Glu Gln Gly Asn Val Ser Thr Met Gly Phe Pro
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Phe Glu Lys Ala Ser Tyr Gly Gly Thr Val Val Lys Glu Trp Leu Asn
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Gly Ala Asn Ala Met Lys Leu Ser Pro Gly Gln Ser Ile Gly Ile Pro
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Asn Pro Ile Phe Gln Gln Ile Asn Phe Ala Ser Thr Val Asp Asn Asn
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Ser Tyr Thr Thr Gly Ser Ala Asn Leu Ile Pro Ala Ile Ala Pro Leu
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Trp Ser Thr Ser Ser Asp Lys Ala Leu Thr Gly Ser Met Ser Ile Thr
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Ser Asn Thr Gln Asp Ala Leu Ala Thr Asp Val Ser Asp His Asp Ile
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Ser Lys Ala Arg Asn Leu Leu Val Gly Gly Asn Phe Asp Asn Leu Asp
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Ser Ile Asp Val Gly Ala Leu Asp Val Asp Thr Asn Pro Gly Ile Glu
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Gln Val	Val Leu Glu	Asp Gly	Lys Arg Val	Leu Arg	Leu Pro Asp
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Ile Pro Glu Val Gly Thr Val Ala Ser Ala Ala Ser Thr Ile Val Ser
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Phe Ile Trp Pro Lys Ile Phe Gly Asp Lys Pro Asn Ala Lys Asn Ile
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Phe Glu Glu Leu Lys Pro Gln Ile Glu Ala Leu Ile Gln Gln Asp Ile
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Thr Asn Tyr Gln Asp Ala Ile Asn Gln Lys Lys Phe Asp Ser Leu Gln
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Lys Thr Ile Asn Leu Tyr Thr Val Ala Ile Asp Asn Asn Asp Tyr Val
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Thr Ala Lys Thr Gln Leu Glu Asn Leu Asn Ser Ile Leu Thr Ser Asp
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Ile Ser Ile Phe Ile Pro Glu Gly Tyr Glu Thr Gly Gly Leu Pro Tyr
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Val Asn Ala Glu Lys Leu Gly Phe Ser Asp Lys Glu Val Asp Thr His
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Lys Lys Tyr Ile Lys Met Thr Ile His Asn His Thr Glu Ala Val Ile
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Lys Ala Phe Leu Asn Gly Leu Asp Lys Phe Lys Ser Leu Asp Val Asn
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Ser Tyr Asn Lys Lys Ala Asn Tyr Ile Lys Gly Met Thr Glu Met Val
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Leu Asp Leu Val Ala Leu Trp Pro Thr Phe Asp Pro Asp His Tyr Gln
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Gln Pro Val Pro Lys Asn Met Gln Asn Thr Ser Ser Ser Ile Val Pro
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Phe Ser Tyr Asn Thr Gln Ser Ser Gly Asn Ile Ser Arg Gly Ser Ser
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Arg Asn Ser Phe Tyr Lys Ala Ile Ala Gly Ser Ser Val Leu Val Asn
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Phe Lys Asp Gly Thr Gln Gly Tyr Ala Phe Ala Gln Ala Pro Thr Gly
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Gly Ala Trp Asp His Ser Phe Ile Glu Ser Asp Gly Ala Pro Glu Gly
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His Lys Leu Asn Tyr Ile Tyr Thr Ser Pro Gly Asp Thr Leu Arg Asp
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Ser Thr Glu Lys Ile Lys Gly Phe Pro Ala Glu Lys Gly Tyr Ile Lys
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Leu Asp Arg Ile Glu Phe Val Pro Lys Asp Ser Leu Gln Asp Ser Pro
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Ser Ser Pro Thr Ile Trp Ser Ser Asn Lys His Ser Tyr Ser His Ile
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His Val Asn Asn Gly Asp Met Asn Val Asp Tyr Gly Lys Asp Ser Val
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Ala Asp Gly Leu Asn Phe Asn Lys Ile Thr Ala Thr Ile Pro Ser Asp
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Ala Trp Tyr Ser Gly Thr Ile Thr Ser Met His Leu Phe Asn Asp Asn
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20           25           30

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Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu Trp Ala Thr Ile Gly
 35 40 45

Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val Asn Glu Gln Gln Leu
 50 55 60

Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
 65 70 75 80

Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
 85 90 95

Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
 100 105 110

Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
 115 120 125

Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
 130 135 140

Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
 145 150 155 160

Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
 165 170 175

Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
 180 185 190

Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
 195 200 205

Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
 210 215 220

Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
 225 230 235 240

Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
 245 250 255

Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
 260 265 270

Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
 275 280 285

Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys Ile Ile Gly Met Leu
 290 295 300

Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
 305 310 315 320

Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
 325 330 335

Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
 340 345 350

Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
 355 360 365

Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
 370 375 380

Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp
 385 390 395 400

Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
 405 410 415

Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr
 420 425 430

Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
 435 440 445

Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
 450 455 460

Asp Trp Tyr Asn Asn Ser Asp Trp Tyr Asn Asn
 465 470 475

<210> 9

<211> 1185
 <212> DNA
 <213> *Bacillus thuringiensis*

<400> 9
 atgatttttag ggaatggaaa gactttacca aagcatataa gattagctca tatttttgca 60
 acacagaatt cttcagctaa gaaagacaat cctcttggac cagaggggat gggtactaaa 120
 gacggtttta taatctctaa ggaagaatgg gcatttgtgc aggcctatgt gactacaggc 180
 actggtttac ctatcaatga cgatgagatg cgtagacatg ttgggttacc atcacgcatt 240
 caaattcctg atgattttta tcaattatat aagggtttata atgaagataa acatttatgc 300
 agttgggtgga atgggtttctt gtttccatta gttcttaaaa cagctaataa tatttccgct 360
 tacggattta aatgtgctgg aaaggggtgcc actaaaggat attatgaggt catgcaagac 420
 gatgtagaaa atatttcaga taatggttat gataaagttg cacaagaaaa agcacataag 480
 gatctgcagg cgcgttgtaa aatccttatt aaggaggctg atcaatataa agctgcagcg 540
 gatgatgttt caaaacattt aaacacattt cttaaaggcg gtcaagattc agatggcaat 600
 gatgttattg gcgtagaggc tgttcaagta caactagcac aagtaaaaga taatcttgat 660
 ggcctatatg gcgacaaaag cccaagacat gaagagttac taaagaaagt agacgacctg 720
 aaaaaagagt tggaagctgc tattaaagca gagaatgaat tagaaaagaa agtgaaaatg 780
 agttttgctt taggaccatt acttggattt gttgtatatg aaatcttaga gctaactgcg 840
 gtcaaaagta tacacaagaa agttgaggca ctacaagccg agcttgacac tgctaattgat 900
 gaactcgaca gagatgtaaa aatcttagga atgatgaata gcattgacac tgatattgac 960
 aacatgttag agcaaggta gcaagctctt gttgtattta gaaaaattgc aggcatttgg 1020
 agtggtataa gtcttaatat cggcaatctt cgagaaacat ctttaaaaga gatagaagaa 1080
 gaaaatgatg acgatgcact gtatattgag cttgggtgatg ccgctgggtca atggaaagag 1140
 atagccgagg aggcacaatc ctttgtacta aatgcttata ctcct 1185

<210> 10
 <211> 395
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 10

Met Ile Leu Gly Asn Gly Lys Thr Leu Pro Lys His Ile Arg Leu Ala
 1 5 10 15

His Ile Phe Ala Thr Gln Asn Ser Ser Ala Lys Lys Asp Asn Pro Leu
 20 25 30

Gly Pro Glu Gly Met Val Thr Lys Asp Gly Phe Ile Ile Ser Lys Glu
 35 40 45

Glu Trp Ala Phe Val Gln Ala Tyr Val Thr Thr Gly Thr Gly Leu Pro
 50 55 60

Ile Asn Asp Asp Glu Met Arg Arg His Val Gly Leu Pro Ser Arg Ile
 65 70 75 80

Gln Ile Pro Asp Asp Phe Asn Gln Leu Tyr Lys Val Tyr Asn Glu Asp
 85 90 95

Lys His Leu Cys Ser Trp Trp Asn Gly Phe Leu Phe Pro Leu Val Leu
 100 105 110

Lys Thr Ala Asn Asp Ile Ser Ala Tyr Gly Phe Lys Cys Ala Gly Lys
 115 120 125

Gly Ala Thr Lys Gly Tyr Tyr Glu Val Met Gln Asp Asp Val Glu Asn
 130 135 140

Ile Ser Asp Asn Gly Tyr Asp Lys Val Ala Gln Glu Lys Ala His Lys
 145 150 155 160

Asp Leu Gln Ala Arg Cys Lys Ile Leu Ile Lys Glu Ala Asp Gln Tyr
 165 170 175

Lys Ala Ala Ala Asp Asp Val Ser Lys His Leu Asn Thr Phe Leu Lys
 180 185 190

Gly Gly Gln Asp Ser Asp Gly Asn Asp Val Ile Gly Val Glu Ala Val
 195 200 205

Gln Val Gln Leu Ala Gln Val Lys Asp Asn Leu Asp Gly Leu Tyr Gly
 210 215 220

Asp Lys Ser Pro Arg His Glu Glu Leu Leu Lys Lys Val Asp Asp Leu
 225 230 235 240

Lys Lys Glu Leu Glu Ala Ala Ile Lys Ala Glu Asn Glu Leu Glu Lys
 245 250 255

Lys Val Lys Met Ser Phe Ala Leu Gly Pro Leu Leu Gly Phe Val Val
 260 265 270

Tyr Glu Ile Leu Glu Leu Thr Ala Val Lys Ser Ile His Lys Lys Val
 275 280 285

Glu Ala Leu Gln Ala Glu Leu Asp Thr Ala Asn Asp Glu Leu Asp Arg
 290 295 300

Asp Val Lys Ile Leu Gly Met Met Asn Ser Ile Asp Thr Asp Ile Asp
 305 310 315 320

Asn Met Leu Glu Gln Gly Glu Gln Ala Leu Val Val Phe Arg Lys Ile
 325 330 335

Ala Gly Ile Trp Ser Val Ile Ser Leu Asn Ile Gly Asn Leu Arg Glu
 340 345 350

Thr Ser Leu Lys Glu Ile Glu Glu Glu Asn Asp Asp Ala Leu Tyr
 355 360 365

Ile Glu Leu Gly Asp Ala Ala Gly Gln Trp Lys Glu Ile Ala Glu Glu
 370 375 380

Ala Gln Ser Phe Val Leu Asn Ala Tyr Thr Pro
 385 390 395

<210> 11
 <211> 2412
 <212> DNA
 <213> *Bacillus thuringiensis*

<400> 11
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 accgttaaag agctcaagga agcatgggaa gcgttcctaaa aaaacggaag tttctcatta 180
 gcagctcttg aaaagggatt tgatgcagca atcggaggag gatcctttga ttatttaggt 240
 ttagttcaag cgggcctagg attagttggt acgctaggcg ccgcaatccc tgggtgtttca 300
 gtggcagtgc ctcttattag catgcttggt ggtgtttttt ggccaaaggg cacaacaac 360

caagaaaacc ttattacagt tattgataag gaagttcaga gaatactaga tgaaaagcta	420
tctgatcagt taataaagaa attgaacgca gattttaatg cttttacgga cctagtaact	480
cgtttggaag aagtaataat agatgcaact ttcgagaatc acaagcctgt actacaagta	540
agtaaataca attatatgaa agtggattca gcatatttct caacaggagg tattcttact	600
cttggcatga gtgattttct tactgatacc tattcaaagc ttaccttccc attatatgta	660
ctaggcgcaa ctatgaaact ttcagcatat catagttata tacaattcgg aaatacatgg	720
cttaataaag tttatgattt atcatcagat gagggaaaaa caatgtcgca ggcttttagca	780
cgagctaaac agcatatgag ccaagacata gcattttata caagccaagc tttaaacatg	840
tttactggga atctcccttc attatcatct aataaatatg caattaatga ctataatgta	900
tacactcgag caatgggtatt gaatggctta gatatagtag caacatggcc taccctatat	960
ccagatgact attcgtctca gataaaactg gagaaaacac gcgtgatctt ttcagatatg	1020
gtcgggcaaa gtgagagtag agatggcagc gtaacgatta aaaatatttt tgacaataca	1080
gattcacatc aacatggatc cataggtctc aattcaatct cttatttccc agatgagtta	1140
cagaaagcac aacttcgcat gtatgattat aatcacaaac cttattgtac ggactgtttc	1200
tgctggccgt atggagtgat tttaaactat aacaagaata cctttagata tggcgataat	1260
gatccaggtc tttcaggaga cgttcaactc ccagcaccta tgagtgtagt taatgccccaa	1320
actcaaacag cccaatatac agatggagaa aacatatgga cagatactgg ccgcagttgg	1380
ctttgtactc tacgtggcta ctgtactaca aactgttttc caggaagagg ttgttataat	1440
aatagtactg gatatggaga aagttgcaat caatcacttc caggtcaaaa aatacatgca	1500
ctatatcctt ttacacaaac aaatgtgctg ggacaatcag gcaaactagg attgctagca	1560
agtcatatc catatgacct aagtccgaac aatacgattg gtgacaaaga tacagattct	1620
acgaatattg tcgcaaaagg aattccagtg gaaaaagggc atgcatccag tggacaaaaa	1680
gttgaaatta tacgagagtg gataaatggc gcgaatgtag ttcaattatc tccaggccaa	1740
tcttggggaa tggattttac caatagcaca ggtgggtcaat atatggtccg ctgtcgatat	1800
gcaagtacaa acgatactcc aatctttttt aatttagtgt atgacggggg atcgaatcct	1860
atttataacc agatgacatt ccctgctaca aaagagactc cagctcacga ttcagtagat	1920
aacaagatac taggcataaa aggaataaat ggaaattatt cactcatgaa tgtaaaagat	1980
tctgtcgaac ttccatctgg gaaatttcat gtttttttca caaataatgg atcatctgct	2040

atttatttag atcgacttga gtttggtcct ttagatcaac cagcagcgcc aacacagtca 2100
 acacaaccaa ttaattatcc tatcacaagt aggttacctc atcgttccgg agaaccacct 2160
 gcaataatat gggagaaatc agggaatggt cgcgggaatc aactaactat atcggcacaa 2220
 ggtggtccag aaaattccca aatatatctt tcggtgggtg gcgatcgcca aatttttagac 2280
 cgtagcaacg gatttaaatt agttaattac tcacctactt attctttcac taacattcag 2340
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 tctaattctat aa 2412

<210> 12
 <211> 803
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 12

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Ala Gly Val Pro Thr Ser Asn Thr Gly Ser Pro Ile Gly Asn Ala Gly
 20 25 30

Asn Gln Phe Asp Gln Phe Glu Gln Thr Val Lys Glu Leu Lys Glu Ala
 35 40 45

Trp Glu Ala Phe Gln Lys Asn Gly Ser Phe Ser Leu Ala Ala Leu Glu
 50 55 60

Lys Gly Phe Asp Ala Ala Ile Gly Gly Gly Ser Phe Asp Tyr Leu Gly
 65 70 75 80

Leu Val Gln Ala Gly Leu Gly Leu Val Gly Thr Leu Gly Ala Ala Ile
 85 90 95

Pro Gly Val Ser Val Ala Val Pro Leu Ile Ser Met Leu Val Gly Val
 100 105 110

Phe Trp Pro Lys Gly Thr Asn Asn Gln Glu Asn Leu Ile Thr Val Ile
 115 120 125

Asp Lys Glu Val Gln Arg Ile Leu Asp Glu Lys Leu Ser Asp Gln Leu
 130 135 140

Ile Lys Lys Leu Asn Ala Asp Leu Asn Ala Phe Thr Asp Leu Val Thr
 145 150 155 160

Arg Leu Glu Glu Val Ile Ile Asp Ala Thr Phe Glu Asn His Lys Pro
 165 170 175

Val Leu Gln Val Ser Lys Ser Asn Tyr Met Lys Val Asp Ser Ala Tyr
 180 185 190

Phe Ser Thr Gly Gly Ile Leu Thr Leu Gly Met Ser Asp Phe Leu Thr
 195 200 205

Asp Thr Tyr Ser Lys Leu Thr Phe Pro Leu Tyr Val Leu Gly Ala Thr
 210 215 220

Met Lys Leu Ser Ala Tyr His Ser Tyr Ile Gln Phe Gly Asn Thr Trp
 225 230 235 240

Leu Asn Lys Val Tyr Asp Leu Ser Ser Asp Glu Gly Lys Thr Met Ser
 245 250 255

Gln Ala Leu Ala Arg Ala Lys Gln His Met Arg Gln Asp Ile Ala Phe
 260 265 270

Tyr Thr Ser Gln Ala Leu Asn Met Phe Thr Gly Asn Leu Pro Ser Leu
 275 280 285

Ser Ser Asn Lys Tyr Ala Ile Asn Asp Tyr Asn Val Tyr Thr Arg Ala
 290 295 300

Met Val Leu Asn Gly Leu Asp Ile Val Ala Thr Trp Pro Thr Leu Tyr
 305 310 315 320

Pro Asp Asp Tyr Ser Ser Gln Ile Lys Leu Glu Lys Thr Arg Val Ile
 325 330 335

Phe Ser Asp Met Val Gly Gln Ser Glu Ser Arg Asp Gly Ser Val Thr
 340 345 350

Ile Lys Asn Ile Phe Asp Asn Thr Asp Ser His Gln His Gly Ser Ile
 355 360 365

Gly Leu Asn Ser Ile Ser Tyr Phe Pro Asp Glu Leu Gln Lys Ala Gln
 370 375 380

Leu Arg Met Tyr Asp Tyr Asn His Lys Pro Tyr Cys Thr Asp Cys Phe
 385 390 395 400

Cys Trp Pro Tyr Gly Val Ile Leu Asn Tyr Asn Lys Asn Thr Phe Arg
 405 410 415

Tyr Gly Asp Asn Asp Pro Gly Leu Ser Gly Asp Val Gln Leu Pro Ala
 420 425 430

Pro Met Ser Val Val Asn Ala Gln Thr Gln Thr Ala Gln Tyr Thr Asp
 435 440 445

Gly Glu Asn Ile Trp Thr Asp Thr Gly Arg Ser Trp Leu Cys Thr Leu
 450 455 460

Arg Gly Tyr Cys Thr Thr Asn Cys Phe Pro Gly Arg Gly Cys Tyr Asn
 465 470 475 480

Asn Ser Thr Gly Tyr Gly Glu Ser Cys Asn Gln Ser Leu Pro Gly Gln
 485 490 495

Lys Ile His Ala Leu Tyr Pro Phe Thr Gln Thr Asn Val Leu Gly Gln
 500 505 510

Ser Gly Lys Leu Gly Leu Leu Ala Ser His Ile Pro Tyr Asp Leu Ser
 515 520 525

Pro Asn Asn Thr Ile Gly Asp Lys Asp Thr Asp Ser Thr Asn Ile Val
 530 535 540

Ala Lys Gly Ile Pro Val Glu Lys Gly Tyr Ala Ser Ser Gly Gln Lys
 545 550 555 560

Val Glu Ile Ile Arg Glu Trp Ile Asn Gly Ala Asn Val Val Gln Leu
 565 570 575

Ser Pro Gly Gln Ser Trp Gly Met Asp Phe Thr Asn Ser Thr Gly Gly
 580 585 590

Gln Tyr Met Val Arg Cys Arg Tyr Ala Ser Thr Asn Asp Thr Pro Ile
 595 600 605

Phe Phe Asn Leu Val Tyr Asp Gly Gly Ser Asn Pro Ile Tyr Asn Gln
 610 615 620

Met Thr Phe Pro Ala Thr Lys Glu Thr Pro Ala His Asp Ser Val Asp
 625 630 635 640

Asn Lys Ile Leu Gly Ile Lys Gly Ile Asn Gly Asn Tyr Ser Leu Met
 645 650 655

Asn Val Lys Asp Ser Val Glu Leu Pro Ser Gly Lys Phe His Val Phe
 660 665 670

Phe Thr Asn Asn Gly Ser Ser Ala Ile Tyr Leu Asp Arg Leu Glu Phe
 675 680 685

Val Pro Leu Asp Gln Pro Ala Ala Pro Thr Gln Ser Thr Gln Pro Ile
 690 695 700

Asn Tyr Pro Ile Thr Ser Arg Leu Pro His Arg Ser Gly Glu Pro Pro
 705 710 715 720

Ala Ile Ile Trp Glu Lys Ser Gly Asn Val Arg Gly Asn Gln Leu Thr
 725 730 735

Ile Ser Ala Gln Gly Val Pro Glu Asn Ser Gln Ile Tyr Leu Ser Val
 740 745 750

Gly Gly Asp Arg Gln Ile Leu Asp Arg Ser Asn Gly Phe Lys Leu Val
 755 760 765

Asn Tyr Ser Pro Thr Tyr Ser Phe Thr Asn Ile Gln Ala Ser Ser Ser
 770 775 780

Asn Leu Val Asp Ile Thr Ser Gly Thr Ile Thr Gly Gln Val Gln Val
 785 790 795 800

Ser Asn Leu

<210> 13

<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Probe

<400> 13

Arg Glu Trp Ile Asn Gly Ala Asn
1 5

<210> 14
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> DNA coding for probe of SEQ ID NO:13

<400> 14
agartrkwtw aatggwgckm aw

22

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Probe

<400> 15

Pro Thr Phe Asp Pro Asp Leu Tyr
1 5

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA coding for probe of SEQ ID NO:15

<220>
<221> misc_feature
<222> (3)..(3)
<223> any nucleotide

<400> 16
ccnacytttk atccagatsw ytat

24

<210> 17
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal amino acid sequence of 17a.

<400> 17

Ala Ile Leu Asn Glu Leu Tyr Pro Ser Val Pro Tyr Asn Val
1 5 10

<210> 18
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal amino acid sequence of 17b.

<400> 18

Ala Ile Leu Asn Glu Leu Tyr Pro Ser Val Pro Tyr Asn Val
1 5 10

<210> 19
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal amino acid sequence of 52A1.

<400> 19

Met Ile Ile Asp Ser Lys Thr Thr Leu Pro Arg His Ser Leu Ile Asn
1 5 10 15

Thr

<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal amino acid sequence of 63B.

<400> 20

Gln Leu Gln Ala Gln Pro Leu Ile Pro Tyr Asn Val Leu Ala
1 5 10

<210> 21
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal amino acid sequence of 69D1.

<400> 21

Met Ile Leu Gly Asn Gly Lys Thr Leu Pro Lys His Ile Arg Leu Ala
1 5 10 15

His Ile Phe Ala Thr Gln Asn Ser
20

<210> 22
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal amino acid sequence of 33F2.

<400> 22

Ala Thr Leu Asn Glu Val Tyr Pro Val Asn
1 5 10

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Internal amino acid sequence for 63B.

<400> 23

Val Gln Arg Ile Leu Asp Glu Lys Leu Ser Phe Gln Leu Ile Lys
1 5 10 15

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide derived from 17.

<400> 24
gcaatttttaa atgaattata tcc 23

<210> 25
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide probe designed from the N-terminal amino acid sequence of 52A1.

<400> 25
atgattattg attctaaaac aacattacca agacattcwt taatwaatac watwaa 56

<210> 26
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe designated as 69D1-D.

<400> 26
aaacatatta gattagcaca tatttttgca acacaaaa 38

<210> 27
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward oligonucleotide primer from 63B.

<400> 27
caaytacaag cwcaacc 17

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse oligonucleotide primer from 63B.

<400> 28
ttcatctaaa attctttgwa c 21

<210> 29
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> Nematode (NEMI) variant of region 5 of Hofte and Whiteley.

<400> 29

Leu Asp Arg Ile Gln Phe Ile Pro
1 5

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse complement primer to SEQ ID NO:29.

<400> 30

aggaacaaay tcaakwcgrt cta

23

<210> 31

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide

<400> 31

Tyr Ile Asp Lys Ile Glu Phe Ile Pro
1 5

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide coding for the peptide of SEQ ID NO:31.

<400> 32

tggaataaat tcaattykrt cwa

23

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide probe 33F2A.

<400> 33
 gcwacwttaa atgaagtwta t 21

<210> 34
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide probe 33F2B.

<400> 34
 aatgaagtwat atccwgtwaa t 21

<210> 35
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Reverse primer.

<400> 35
 gcaagcggcc gcttatggaa taaattcaat tykrtcwa 38

<210> 36
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer.

<400> 36
 tgattttwmt caattatatr akgtttat 28

<210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Probe

<400> 37
 aagagttayt araraaagta 20

<210> 38
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Probe

<400> 38

ttaggaccat trytwggatt tgttgwtat gaaat

35

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe

<400> 39

gayagagatg twaaaatywt aggaatg

27

<210> 40

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer.

<400> 40

ttmttaaawc wgctaatgat att

23